

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> TRANSPORTER GENES

<130> C2-906DP1PCT

<140>

<141>

Sub A1 > <150> JP 9-260972

JP 10-156660

<151> 1997-9-8

1998-5-20

<160> 28

<210> 1

<211> 551

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Asp Tyr Asp Glu Val Ile Ala
1 5

Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
10 15 20 25

Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
30 35 40

Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
45 50 55

Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
60 65 70

Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
75 80 85

Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu

Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
 330 335 340 345

Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
 350 355 360

Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
 365 370 375

Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Arg
 380 385 390

Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
 395 400 405

Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
 410 415 420 425

Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
 430 435 440

Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg
 445 450 455

Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
 460 465 470

Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
 475 480 485

Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
 490 495 500 505

Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
 510 515 520

Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
 525 530 535

Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
 540 545 550

Sub A1

<210> 2
<211> 2135
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (147)..(1799)

<400> 2
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cttggggagc gccccagcta caagacactg tcctgagaac gctgtcatca cccgtagttg 120

caagtttcgg agcggcagtg ggaagc atg cg gac tac gac gag gtg atc gcc 173
Met Arg Asp Tyr Asp Glu Val Ile Ala
1 5

ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc 221
Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
10 15 20 25

agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc 269
 Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
 30 35 40

ctg gcg ggg acc ccg gag cac cgc tgt cga gtg ccg gac gcc gcg aac 317
Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
45 50 55

ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg ~~cg~~ ctg cg~~g~~ gac 365
Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
60 65 70

ggc cgc gag gtg ccc cac agc tgc agc cgc tac cgg ctc gcc acc atc 413
Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
75 80 85

gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg 461
 Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
 90 95 100 105

ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag 509

Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
 110 115 120

gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag 557
 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
 125 130 135

gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg 605
 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
 140 145 150

ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg 653
 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
 155 160 165

aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc 701
 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
 170 175 180 185

ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc 749
 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
 190 195 200

atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta 797
 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
 205 210 215

gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta 845
 Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
 220 225 230

gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt 893
 Gly Val Cys Thr Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
 235 240 245

gct tac ttc atc aga gac tgg cgg atg ctg ctg ctg gcg ctg acg gtg 941
 Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Ala Leu Thr Val
 250 255 260 265

ccg gga gtg ctg tgt gtc ccg ctg tgg tgg ttc att cct gaa tct ccc 989
 Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
 270 275 280

SubA1

SubB1

cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc 1037
 Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
 285 290 295

caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt 1085
 Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
 300 305 310

gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att 1133
 Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
 315 320 325

SubA1 >
 ctg gac ctg ttc agg act cgg aat att gcc ata atg acc att atg tct 1181
 Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
 330 335 340 345

ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg 1229
 Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
 350 355 360

gat gct cct aat tta cat gga gat gac tac ctg aac tgt ttc ctc tct 1277
 Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
 365 370 375

gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga 1325
 Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Arg
 380 385 390

acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga 1373
 Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
 395 400 405

ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta 1421
 Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
 410 415 420 425

tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc 1469
 Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
 430 435 440

tcc atg ctg tat gtc ttc act gct gag ctc tac cca acc ctg gtc agg 1517
 Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg
 445 450 455

aac atg gcg gtg ggg gtc aca tcc acg gcc tcc aga gtg ggc agc atc 1565
 Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
 460 465 470

att gcc ccc tac ttt gtt tac ctc ggt gct tac aac aga atg ctg ccc 1613
 Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
 475 480 485

SUB A1 >
 tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt 1661
 Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
 490 495 500 505

ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag 1709
 Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
 510 515 520

atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca 1757
 Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
 525 530 535

atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc 1799
 Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
 540 545 550

tgaaaaaaaata tctaccccat ttgggtgaagt gaaaaacaga aaaataagac cctgtggaga 1859

aattcgttgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaaccttgc 1919

tatcaagaaa tgctcgcat acagtaaact ctggatgatt cttccagata atgtccttgc 1979

tttacaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg 2039

taagatgtct tgaaaacatg ttagtcaagg actggtaaaa tacatataaa gattaacact 2099

catttcaat catabaaata ctatccaaat aaaaat 2135

<210> 3
 <211> 557
 <212> PRT
 <213> Homo sapiens

 <400> 3

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Pro	Phe	Gln	Arg	Leu	Ile	Phe	Phe	Leu	Leu	Ser	Ala	Ser	Ile	Ile	Pro
					20					25			30		
Asn	Gly	Phe	Thr	Gly	Leu	Ser	Ser	Val	Phe	Leu	Ile	Ala	Thr	Pro	Glu
					35					40			45		
His	Arg	Cys	Arg	Val	Pro	Asp	Ala	Ala	Asn	Leu	Ser	Ser	Ala	Trp	Arg
					50					55			60		
Asn	His	Thr	Val	Pro	Leu	Arg	Leu	Arg	Asp	Gly	Arg	Glu	Val	Pro	His
					65					70			75		
Ser	Cys	Arg	Arg	Tyr	Arg	Leu	Ala	Thr	Ile	Ala	Asn	Phe	Ser	Ala	Leu
					80					85			90		95
Gly	Leu	Glu	Pro	Gly	Arg	Asp	Val	Asp	Leu	Gly	Gln	Leu	Glu	Gln	Glu
					100					105			110		
Ser	Cys	Leu	Asp	Gly	Trp	Glu	Phe	Ser	Gln	Asp	Val	Tyr	Leu	Ser	Thr
					115					120			125		
Ile	Val	Thr	Glu	Trp	Asn	Leu	Val	Cys	Glu	Asp	Asp	Trp	Lys	Ala	Pro
					130					135			140		
Leu	Thr	Ile	Ser	Leu	Phe	Phe	Val	Gly	Val	Leu	Leu	Gly	Ser	Phe	Ile
					145					150			155		
Ser	Gly	Gln	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Asn	Val	Leu	Phe	Val
					160					165			170		175
Thr	Met	Gly	Met	Gln	Thr	Gly	Phe	Ser	Phe	Leu	Gln	Ile	Phe	Ser	Lys
					180					185			190		
Asn	Phe	Glu	Met	Phe	Val	Val	Leu	Phe	Val	Leu	Val	Gly	Met	Gly	Gln
					195					200			205		
Ile	Ser	Asn	Tyr	Val	Ala	Ala	Phe	Val	Leu	Gly	Thr	Glu	Ile	Leu	Gly
					210					215			220		
Lys	Ser	Val	Arg	Ile	Ile	Phe	Ser	Thr	Leu	Gly	Val	Cys	Ile	Phe	Tyr

Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
 465 470 475

Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met
 480 485 490 495

Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
 500 505 510

Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
 515 520 525

Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys
 530 535 540

Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe
 545 550 555

<210> 4

<211> 1831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (124)..(1794)

<400> 4

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ggc atg cgg gac tac gac gag gtg acc gcc ttc ctg ggc gag tgg ggg 168

Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly

1

5

10

15

ccc ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc 216

Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro

20

25

30

aat ggc ttc acc ggc ctg tcc tcc gtg ttc ctg ata ggc acc ccg gag 264

Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu

SubA1

A

35 40 45

cac cgc tgc egg gtg ccg gac gcc gcg aac ctg agc agc gcc tgg cgc 312
 His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
 50 55 60

aac cac act gtc cca ctg cgg ctg cgg gac ggc cgc gag gtg ccc cac 360
 Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
 65 70 75

agc tgc cgc cgc tac cgg ctc gcc acc atc gcc aac ttc tcg gcg ctc 408
 Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
 80 85 90 95

ggg ctg gag ccg ggg cgc gac gtg gac ctg ggg cag ctg gag cag gag 456
 Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
 100 105 110

agc tgt ctg gat ggc tgg gag ttc agt cag gac gtc tac ctg tcc acc 504
 Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
 115 120 125

att gtg acc gag tgg aac ctg gtg tgt gag gac gac tgg aag gcc cca 552
 Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
 130 135 140

ctc aca atc tcc ttg ttc gtc ggt gtg ctg ttg ggc fcc ttc att 600
 Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
 145 150 155

tca ggg cag ctg tca gac agg ttt ggc cgg aag aat gtg ctg ttc gtg 648
 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
 160 165 170 175

acc atg ggc atg cag aca ggc ttc agc ttc ctg cag atc ttc tcg aag 696
 Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
 180 185 190

aat ttt gag atg ttt gtc gtg ctg ttt gtc ctt gta ggc atg ggc cag 744
 Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
 195 200 205

atc tcc aac tat gtg gca gca ttt gtc ctg ggg aca gaa att ctt ggc 792

Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
 210 215 220

aag tca gtt cgt ata ata ttc tct acg tta gga gtg tgc ata ttt tat 840
 Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr
 225 230 235

gca ttt ggc tac atg gtg ctg cca ctg ttt gct tac ttc atc cga gac 888
 Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp
 240 245 250 255

Sub A1
 tgg cgg atg ctg ctg gtg gcg ctg acg atg ccg ggg gtg ctg tgc gtg 936
 Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
 260 265 270

gca ctc tgg tgg ttc atc ctc gag tcc ccc cga tgg ctc atc tct cag 984
 Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
 275 280 285

gga cga ttt gaa gag gca gag gtg atc atc cgc aag gct gcc aaa gcc 1032
 Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
 290 295 300

aat ggg att gtt gtg cct tcc act atc ttt gac ccg agt gag tta caa 1080
 Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
 305 310 315

gac cta agt tcc aag aag cag cag tcc cac aac att ctg gat ctg ctt 1128
 Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
 320 325 330 335

cga acc tgg aat atc cgg atg gtc acc atc atg tcc ata atg ctg tgg 1176
 Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
 340 345 350

atg acc ata tca gtg ggc tat ttt ggg ctt tcg ctt gat act cct aac 1224
 Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
 355 360 365

ttg cat ggg gac atc ttt gtg aac tgc ttc ctt tca gcg atg gtt gaa 1272
 Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu
 370 375 380

gtc cca gca tat gtg ttg gcc tgg ctg ctg ctg caa tat ttg ccc cgg 1320
 Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
 385 390 395

cgc tat tcc atg gcc act gcc ctc ttc ctg ggt ggc agt gtc ctt ctc 1368
 Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
 400 405 410 415

ttc atg cag ctg gta ccc cca gac ttg tat tat ttg gct aca gtc ctg 1416
 Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
 420 425 430

SubA1
 gtg atg gtg ggc aag ttt gga gtc acg gct gcc ttt tcc atg gtc tac 1464
 Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
 435 440 445

gtg tac aca gcc gag ctg tat ccc aca gtg gtg aga aac atg ggt gtg 1512
 Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
 450 455 460

gga gtc agc tcc aca gca tcc cgc ctg ggc agc atc ctg tct ccc tac 1560
 Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
 465 470 475

ttc gtt tac ctt ggt gcc tac gac cgc ttc ctg ccc tac att ctc atg 1608
 Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met
 480 485 490 495

gga agt ctg acc atc ctg aca gcc atc ctc acc ttg ttt ctc cca gag 1656
 Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
 500 505 510

agc ttc ggt acc cca ctc cca gac acc att gac cag atg cta aga gtc 1704
 Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
 515 520 525

aaa gga atg aaa cac aga aaa act cca agt cac aca agg atg tta aaa 1752
 Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys
 530 535 540

gat ggt caa gaa agg ccc aca atc ctt aaa agc aca gcc ttc 1794
 Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe
 545 550 555

taacatcgct tccagtaagg gagaaactga agaggaa 1831

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

Sub A17

<400> 5

ctaatacgac tcactatagg gc

22

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 6

tgttagcgtga agacgacaga a

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 7

tcgagcggcc gcccgggcag gt

22

<210> 8

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 8

agggcggtggt gcggaggggcg gt

22

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

Sub A1

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 9

ctttttagca agttcagcct

20

A

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 10

agaggtggct tatgagtatt tctt

24

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 11

ccagggttt cccagtcacg ac

22

~~<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence~~

~~<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 12
tcacacagga aacagctatg ac~~

22

~~<210> 13
<211> 24
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<213> Artificial Sequence~~

~~<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 13
gtgctgttgg gctccttcat ttca~~

24

~~<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence~~

~~<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 14
agctgcatga agagaaggac actg~~

24

~~<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence~~

~~<220>~~

SUBMITTED FOR EXAMINATION

~~<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 15~~

~~agcatcctgt ctccctactt cgtt~~

24

~~<210> 16~~

~~<211> 33~~

~~<212> DNA~~

~~<213> Artificial Sequence~~

Sub A1

~~<220>~~

~~<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 16~~

~~gatggatccc ggacggtctt gggtcgcatg ctg~~

33

~~<210> 17~~

~~<211> 33~~

~~<212> DNA~~

~~<213> Artificial Sequence~~

~~<220>~~

~~<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 17~~

~~gatggatcca aatgctgccatagttgga gat~~

33

~~<210> 18~~

~~<211> 33~~

~~<212> DNA~~

~~<213> Artificial Sequence~~

~~<220>~~

~~<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence~~

~~<400> 18~~

~~gatggatcca tgggcatgca gacaggcttc agc~~

33

~~<210> 19~~

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 19

gatggatcct tcctcttcag tttctccctt act

33

Sub A1

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 20

cgcgccgaat cgctgaatcc ttcc

24

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 21

aggctttga tttgttctgt tgag

24

<210> 22

<211> 553

<212> PRT

<213> Mus musculus

<400> 22

Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro

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 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45
 Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
 50 55 60
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
 65 70 75 80
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
 85 90 95
 Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
 115 120 125
 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
 130 135 140
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
 145 150 155 160
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
 165 170 175
 Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
 180 185 190
 Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gln Gln Ile
 195 200 205
 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240

Le Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
 260 265 270

Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285

Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300

Sub A1
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320

Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335

Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350

Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365

His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380

Pro Ala Tyr Phe Thr Ala Trp Leu Leu Arg Thr Leu Pro Arg Arg
 385 390 395 400

Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
 405 410 415

Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
 420 425 430

Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
 435 440 445

Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
 450 455 460

Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
485 470 475 480

Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
485 490 495

Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
500 505 510

Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
515 520 525

Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
530 535 540

Ser Pro Lys Val Leu Ile Thr Ala Phe
545 550

<210> 23

<211> 2083

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (122), (1780)

<400> 23

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tcgctgaatc ctttctctcc acccacctcc ctcacgcaag ctcaggagga gaggtggaaa 120

c atg cgg gac tac gac gag gtg atc gcc ttc ctg ggc gag tgg ggg ccc 169

1 5 10 15
ttc cag cgc ctc atc ttc ttt ctg ctg agc gcc agc atc atc ccc aat

Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
20 25 30

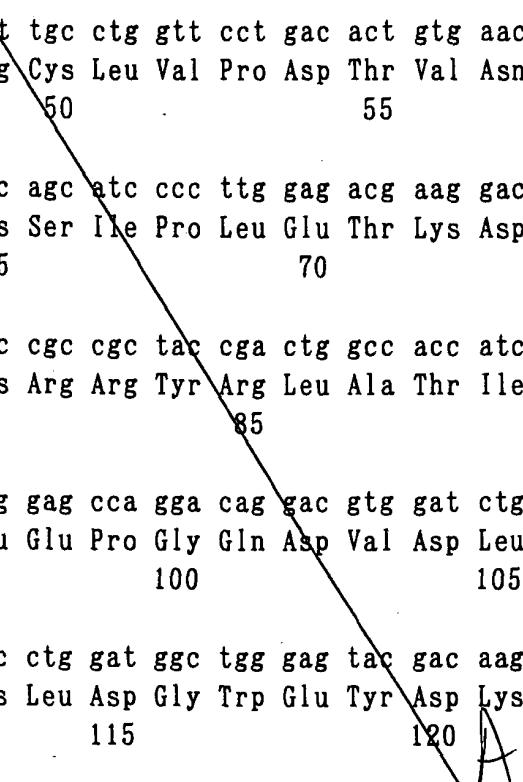
ggc ttc aat ggt atg tca gtc gtg ttc ctg gcg ggg acc ccc gag cac 265
Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His

35 40 45

cgt tgc ctg gtt cct gac act gtg aac ctg agc agc tcc tgg cgc aac 313
 Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
 50 55 60

cac agc atc ccc ttg gag acg aag gac gga cga cag gtg cct cag agc 361
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
 65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gcg atg ggg 409
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
 85 90 95

Sub A1 
 ctg gag cca gga cag gac gtg gat ctg gag cag ctg gag cag gag agc 457
 Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110

tgc ctg gat ggc tgg gag tac gac aag gac atc ttc ctg tcc acc atc 505
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
 115 120 125

gtg aca gag tgg aat ctg gtg tgt gag gat gac tgg aag aca ccc ctc 553
 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
 130 135 140

acc acc tcc ctg ttc ttc gta ggc gtt ctc tgc ggc tcc ttc gtg tct 601
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
 145 150 155 160

ggg cag ctg tca gac agg ttt ggc agg aag aaa gtc ctc ttt gca acc 649
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
 165 170 175

atg gct gtg cag act gga ttc agc ttc gtg cag att ttc tca acc aac 697
 Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
 180 185 190

tgg gag atg ttc act gtg ttg ttt gcc att gtg ggc atg ggc cag atc 745
 Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
 195 200 205

tcc aac tac gtg gtg gcc ttc ata cta gga act gaa atc ctg agc aag 793
 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220

tcc gtt cgc atc atc ttc tcc aca tta gga gtc tgt aca ttt ttt gca 841
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
 225 230 235 240

atc ggc tac atg gtc ctg ccg ctg ttt gca tac ttc atc aga gac tgg 889
 Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

agg atg ctg ctg ctg gcc ctg aca ctg cct ggc ctg ttc tgt gtt ccc 937
 Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
 260 265 270

ctg tgg tgg ttt att cca gaa tct ccc cgg tgg ctg ata tcc cag agg 985
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
 275 280 285

aga ttt gca gag gcc gaa cag atc atc cag aaa gcc gca aag atg aac 1033
 Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
 290 295 300

agc atc gtg gcg cca gca ggg ata ttc gat cct cta gag cta cag gag 1081
 Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
 305 310 315 320

cta aac tcc ttg aag cag cag aaa gtc ata atc ctg gac ctg ttc agg 1129
 Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
 325 330 335

act cgg aac att gcc acc ata acc gtg atg gct gtg atg ctg tgg atg 1177
 Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
 340 345 350

cta acc tca gtg ggt tac ttt gct ctg tct ctc aat gtt cct aat tta 1225
 Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
 355 360 365

cat gga gat gtc tac ctg aac tgc ttc ctc tct ggc ctg att gaa gtt 1273
 His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
 370 375 380

cca gct tac ttc aca gcc tgg ctg cta ctg cga acc ctg cca cgg aga 1321
 Pro Ala Tyr Phe Thr Ala Trp Leu Leu Arg Thr Leu Pro Arg Arg

385	390	395	400
tat att ata gct ggg gtg cta ttc tgg gga gga ggt gtg ctt ctc ttg Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu	405	410	415
atc caa gtg gta cct gaa gat tat aac ttt gtg tcc att gga ctg gtg Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val	420	425	430
atg ctg ggg aaa ttt ggg atc acc tct gcc ttc tcc atg ttg tat gtc Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val	435	440	445
ttc act gcg gag ctc tac cca acc ctg gtc agg aac atg gct gtg ggc Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly	450	455	460
atc acc tcc atg gcc tct cgg gtg ggc agc atc att gcc ccc tat ttc Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe	465	470	475
gtt tac ctg ggc gcc tat aac aga ctc cta ccc tac atc ctc atg ggc Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly	485	490	495
agt ctg act gtc ctc att gga atc atc acg ctt tt ttc cct gaa agt Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser	500	505	510
ttt gga gtg act cta cca gag aac ttg gag cag atg cag aaa gtg aga Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg	515	520	525
ggg ttc aga tgt ggg aaa aaa tca aca gtc tca gtg gac aga gaa gaa Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu	530	535	540
agc ccc aag gtt cta ata act gca ttc taacgagggtt tccaaaggcac Ser Pro Lys Val Leu Ile Thr Ala Phe	545	550	555
ttggcaact gaaaagcaga tgtatacaat gagcagggtg tgatagagca agcctgcaat			1860

cccagcgtc ttgggtgga gacagaagat caggagttca agtcatcct tggctacagc 1920
aggagtgtaa gaccagcctg tcattaccaca agcaaccctg tctcaacaga acaaatcaa 1980
agcctttct gctgaaagg attaacagaa acaatgagca ccaaactgga cttgtggaga 2040
aatgcacact atatcatgaa ttctggcca ctcttccaga tgg 2083

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 24

cccatgcaa caaggacaaa aagc

24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 25

acagaacaga aaagccctca gtca

24

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 26

~~tgttttcgt ggggtgtgctg atgg~~

24

~~<210> 27~~

~~<211> 557~~

~~<212> PRT~~

~~<213> Mus musculus~~

~~<400> 27~~

Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
1 5 10 15

SubA1
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
20 25 30

Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
35 40 45

Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
50 55 60

His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
65 70 75 80

Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
85 90 95

Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
100 105 110

Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
115 120 125

Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
130 135 140

Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
145 150 155 160

Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
165 170 175

Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
180 185 190

Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220

Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
 225 230 235 240

Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
 260 265 270

Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
 275 280 285

Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
 290 295 300

Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
 305 310 315 320

Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg
 325 330 335

Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu
 340 345 350

Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu
 355 360 365

His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val
 370 375 380

Pro Ala Tyr Val Leu Ala Trp Leu Leu Gln Tyr Leu Pro Arg Arg
 385 390 395 400

Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
 405 410 415

SUB A1

DRAFT 10/20/90

Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
 420 425 430

Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
 435 440 445

Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
 450 455 460

Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
 465 470 475 480

Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
 485 490 495

Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
 500 505 510

Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
 515 520 525

Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
 530 535 540

Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
 545 550 555

<210> 28

<211> 1888

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (60)..(1730)

<400> 28

ctcccgcc acgggtgtccc cttattccca tacgggcgt gtgggaggct gaggacggc 59

atg cgg gac tac gac gag gtg acc gcc ttc cta ggc gag tgg ggg ecc 107
 Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro

ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc aat 155
 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 20 25 30

ggc ttc aat ggt atg tcc atc gtg ttc ctg gcg ggg acc ccg gag cac 203
 Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
 35 40 45

cgt tgc ctt gtg cct cac acc gtg aac ctg agc agc gcg tgg cgc aac 251
 Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60

SUBA1 1
 cac agt atc ccg ttg gag acg aag gac gga cga cag gtg cct cag aaa 299
 His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65 70 75 80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gag cta ggg 347
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
 85 90 95

ctg gag ccg ggg cgg gac gtg gac ctg gag cag ctg gag cag gag agc 395
 Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
 100 105 110

tgc ctg gat ggc tgg gag tac gac aag gac gtc ttc ctg tcc acc atc 443
 Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
 115 120 125

gtg aca gag tgg gac ctg gtg tgt aag gat gac tgg aaa gcc cca ctc 491
 Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
 130 135 140

acc acc tcc ttg ttt ttc gtg ggt gtg ctg atg ggc tcc ttc att tca 539
 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
 145 150 155 160

gga cag ctc tca gac agg ttt ggt cgc aag aat gtg ctg ttt ttg acc 587
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
 165 170 175

atg ggc atg cag act ggc ttc agc ttc ctg cag gtc ttc tct gtg aac 635
 Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
 180 185 190

ttc gag atg ttt aca gtg ctt ttt gtc ctt gtt ggc atg ggt cag atc 683
 Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
 195 200 205

tcc aac tac gtg gca gca ttt gtc ctg gga aca gaa att ctt tcc aag 731
 Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
 210 215 220

tca att cga att ata ttc gcc acc tta gga gtt tgc ata ttt tat gcg 779
 Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
 225 230 235 240

SubA1 >
 ttt ggc ttc atg gtg ctg cca ctg ttt gca tac ttc atc aga gac tgg 827
 Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255

agg atg ctg ctg ctg gcg ctc act gtg cca ggg gtg cta tgt ggg gct 875
 Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
 260 265 270

ctc tgg tgg ttc atc cct gag tcc cca cga tgg ctc atc tct caa ggc 923
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
 275 280 285

cga att aaa gag gca gag gtg atc atc cgc aaa gct gcc aaa atc aat 971
 Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
 290 295 300

ggg att gtt gca cct tcc act atc ttc gat cca agt gag tta caa gac 1019
 Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
 305 310 315 320

tta aat tct acg aag cct cag ttg cac cac att tat gat ctg atc cga 1067
 Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg
 325 330 335

aca cgg aat atc agg gtc atc acc atc atg tct ata atc ctg tgg ctg 1115
 Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu
 340 345 350

acc ata tca gtg ggc tat ttt gga cta tct ctt gac act cct aac ttg 1163
 Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu

355 360 365

cat ggg gac atc tat gtg aac tgc ttc cta ctg gcg gct gtt gaa gtc 1211
 His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val
 370 375 380

cca gcc tat gtg ctg gcc tgg ctg ttg cag tac ttg ccc cgg cga 1259
 Pro Ala Tyr Val Leu Ala Trp Leu Leu Gln Tyr Leu Pro Arg Arg
 385 390 395 400

SubA1

tat tct atc tcg gct gcc ctt ttc ctg ggt ggc agt gtc ctt ctc ttc 1307
 Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
 405 410 415

atg cag ctg gtg cct tca gaa ttg ttt tac ttg tcc act gcc ctg gtg 1355
 Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
 420 425 430

atg gtg ggg aag ttt gga atc acc tct gcc tac tcc atg gtc tat gtg 1403
 Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
 435 440 445

tac aca gct gag ctg tac ccc act gtg gtc aga aac atg ggt gtg ggg 1451
 Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
 450 455 460

gtc agc tcc aca gca tcc cgc ctt ggc agc atc ctg tct ccc tac ttt 1499
 Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
 465 470 475 480

gtt tac cta ggt gcc tat gat cgc ttc ctg cct tat att ctc atg gga 1547
 Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
 485 490 495

agt ctg acc atc ctg aca gct atc ctc acc ttg ttc ttc cct gag agc 1595
 Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
 500 505 510

ttt ggt gtc cct ctc cca gat acc att gac cag atg cta agg gtc aaa 1643
 Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
 515 520 525

gga ata aaa cag tgg caa atc caa agc cag aca aga atg caa aaa gat 1691

Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
530 535 540

Sub A1 ggt gaa gaa agc cca asa gtc cta aag agc aca gcc ttc taacaccctg 1740
Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
545 550 555

tccagaaggc aaaaaactga ttggaaacct tcatgttgc agaaaatgctc tccatgactg 1800

agggctttc ttttctgtta accttgcgtc taacatgctc atggatggc gcatctgtcc 1860

tggagagtca ctttcctcta gggacacc 1888

SEQ ID NO:29

CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCGGCAGGT

SEQ ID NO:30

TGTAGCGTGAAGACGACAGAAAGGGCGTGGTGCAGGGCGGT

SEQ ID NO:31

acctggccgg

SEQ ID NO:32

accggccctccg

Sub A1

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100